

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listing of claims in the application.

1-18 and 27-29 (**Cancelled**)

19. (**Currently Amended**) A method for identifying a compound which binds to a SMRTe polypeptide ~~of claim 8~~ comprising:

- a) contacting the polypeptide, or a cell expressing the polypeptide with a test compound; and
- b) determining whether the polypeptide binds to the test compound.

20. (**Original**) The method of claim 19, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

- a) detection of binding by direct detection of test compound/polypeptide binding;
- b) detection of binding using a competition binding assay; and
- c) detection of binding using an assay for SMRTe activity.

21. (**Currently Amended**) A method for modulating the activity of a SMRTe polypeptide ~~of claim 8~~ comprising contacting the polypeptide or a cell expressing the polypeptide with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

22. (**Currently Amended**) A method for identifying a compound which modulates the activity of a SMRTe polypeptide ~~of claim 8~~ comprising:

- a) contacting a the polypeptide ~~of claim 8~~ with a test compound; and
- b) determining the effect of the test compound on the activity of the polypeptide to thereby identify a compound which modulates the activity of the polypeptide.

23. (**Currently Amended**) A method for identifying a compound which modulates the activity of a SMRTe polypeptide ~~of claim 8~~ comprising:

- a) contacting a cell containing a the polypeptide ~~of claim 8~~ with a test compound; and
- b) determining the effect of the test compound on the activity of the polypeptide to interact with a SMRTe target molecule thereby identifying a compound which modulates the activity of the polypeptide.

24. **(Original)** The method of claim 23, wherein said activity is corepression of gene regulation at the level of transcription.

25. **(Original)** The method of claim 23, wherein said SMRTe target molecule is a nuclear hormone receptor.

26. **(Original)** The method of claim 25, wherein said contacting is in the presence of a ligand that binds a nuclear hormone receptor.

30. **(New)** The method as in any one of claims 19, 21, 22, or 23, wherein the SMRTe polypeptide is encoded by a nucleic acid molecule which hybridizes under stringent conditions of 6x sodium chloride / sodium citrate (SSC) at about 45°C followed by at least one wash in 0.2 X SSC, 0.1% SDS at 50-65°C, to a complement of the nucleic acid of SEQ ID NO: 3, and wherein the polypeptide has gene transcription repressor activity.

31. **(New)** The method as in any one of claims 19, 21, 22, or 23, wherein the SMRTe polypeptide is at least 80% identical to a polypeptide sequence selected from the group consisting of SEQ ID NO: 2, amino acid residues 1 to 165 of SEQ ID NO: 2, amino acid residues 165 to 305 of SEQ ID NO: 2, amino acid residues 165 to 665 of SEQ ID NO: 2, amino acid residues 435 to 936 of SEQ ID NO: 2, amino acid residues 725 to 906 of SEQ ID NO: 2, amino acid residues 889 to 973 of SEQ ID NO: 2, and amino acid residues 1 to 1111 of SEQ ID NO: 2, and wherein the polypeptide has gene transcription repressor activity.

32. **(New)** The method as in any one of claims 19, 21, 22, or 23, wherein the SMRTe polypeptide is at least 90% identical to a polypeptide sequence selected from the group consisting of SEQ ID NO: 2, amino acid residues 1 to 165 of SEQ ID NO: 2, amino acid residues 165 to 305 of SEQ ID NO: 2, amino acid residues 165 to 665 of SEQ ID NO: 2, amino acid residues 435 to 936 of SEQ ID NO: 2, amino acid residues 725 to 906 of SEQ ID NO: 2, amino acid residues 889 to 973 of SEQ ID NO: 2, and amino acid residues 1 to 1111 of SEQ ID NO: 2, and wherein the polypeptide has gene transcription repressor activity.

33. **(New)** The method as in any one of claims 19, 21, 22, or 23, wherein the SMRTe polypeptide is at least 95% identical to a polypeptide sequence selected from the group consisting of SEQ ID NO: 2, amino acid residues 1 to 165 of SEQ ID NO: 2, amino acid residues 165 to 305 of SEQ ID NO: 2, amino acid residues 165 to 665 of SEQ ID NO: 2, amino

acid residues 435 to 936 of SEQ ID NO: 2, amino acid residues 725 to 906 of SEQ ID NO: 2, amino acid residues 889 to 973 of SEQ ID NO: 2, and amino acid residues 1 to 1111 of SEQ ID NO: 2.

34. **(New)** The method as in any one of claims 19, 21, 22, or 23, wherein the SMRTe polypeptide comprises a polypeptide sequence selected from the group consisting of SEQ ID NO: 2, amino acid residues 1 to 165 of SEQ ID NO: 2, amino acid residues 165 to 305 of SEQ ID NO: 2, amino acid residues 165 to 665 of SEQ ID NO: 2, amino acid residues 435 to 936 of SEQ ID NO: 2, amino acid residues 725 to 906 of SEQ ID NO: 2, amino acid residues 889 to 973 of SEQ ID NO: 2, and amino acid residues 1 to 1111 of SEQ ID NO: 2.